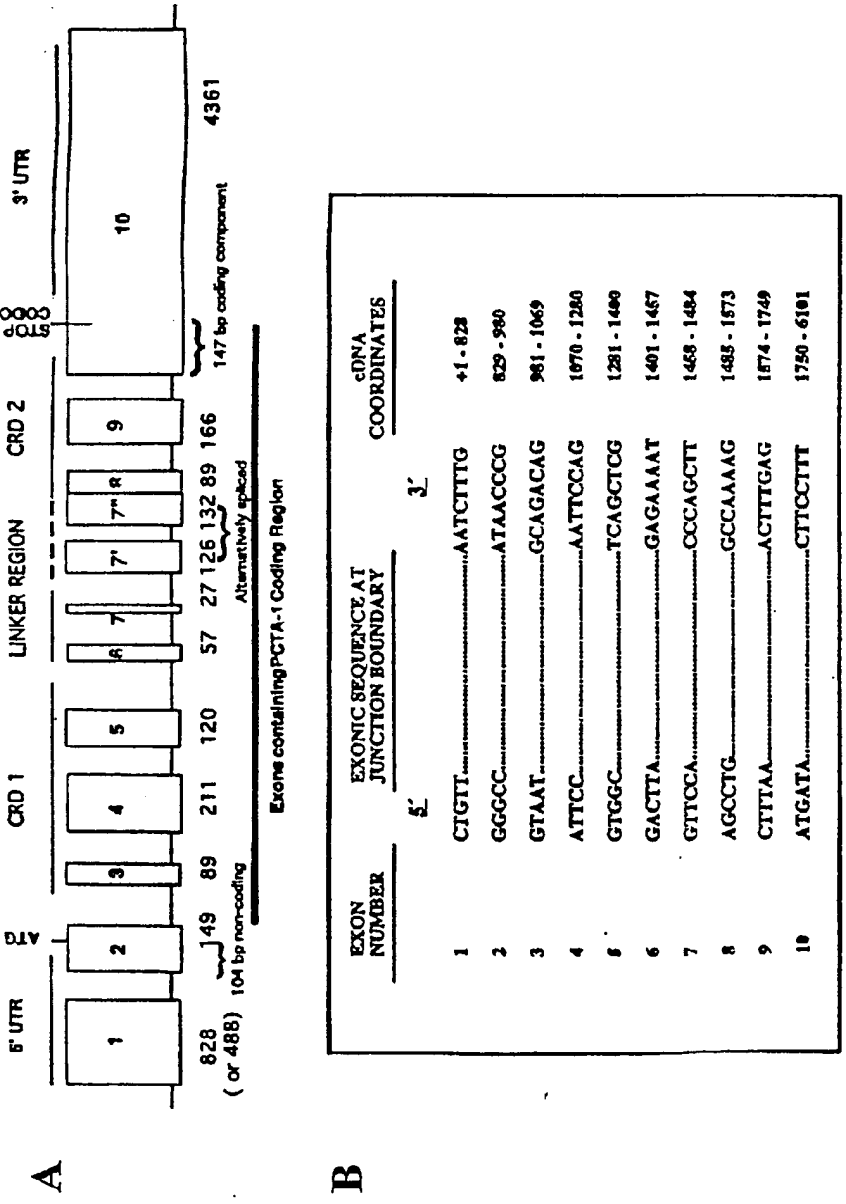
FIGURE 1



B

EXON NUMBER	EXONIC SEQUENCE AT JUNCTION BOUNDARY 5'	3'	cDNA COORDINATES
1	CTGTT.....	.....AATCTTTG	+1 - 828
2	GGGCC.....	.....ATAACCCG	829 - 980
3	GTAAT.....	.....GCAGACAG	981 - 1069
4	ATTCC.....	.....AATTCCAG	1070 - 1280
5	GTGGC.....	.....TCAGCTCG	1281 - 1400
6	GACTTA.....	.....GAGAAAAT	1401 - 1457
7	GTTCCA.....	.....CCCAGCTT	1458 - 1484
8	AGCCTG.....	.....GCCAAAAG	1485 - 1573
9	CTTTAA.....	.....ACTTTGAG	1574 - 1749
10	ATGATA.....	.....CTTCCTTT	1750 - 6101

FIGURE 1 (CONT'D.)

C

Alternate exon 1 (7'): 5'-CCT AGT AAT AGA GGA GGA GAC
ATT TCT AAA ATC GCA CCC AGA ACT GTC TAC ACC AAG
AGC AAA GAT TCG ACT GTC AAT CAC ACT TTG ACT TGC
ACC AAA ATA CCA CCT ATG AAC TAT GTG TCA AAG-3'
Alternate exon 2 (7') 5'-CAG ACT GTC TCT CCC CTC CTG
GGA TTT ACA GGG TCA TGG CTC TGA AAC ATT CTG TAG
(Position 55,56)
TGT TCT TTG GAC ACG AGT TTT CCC TGG AGA TCG CTT
TCT GCA GGC CTA TTG GTC CTG ACT GTG GCT TCT TTT
CAG-5'

D

Exon 2 MMLSLNNLQNIIYNPV

Exon 3 IPFVGTIPDQLDPGTLIVIRGHVPSDADK

Exon 4 FQVDLQNGSSVKPRADVAFHFNPRFKRAGCIVCNTLINEKWGREEITYDTPFKREKSFEIVIMV
LKDKFQ

Exon 5 VAVNGKHTLLYGHRIGPEKIDTLGIYGKVNIHSIGFSFSS

Exon 6 DLQSTQASSLELTEIVREN

Exon 7 VPKSGTPQL

Exon 8 SLPFAARLNTPMGPGRTVVVQGEVNANAKS

Exon 9 FNVDLLAGKSKDIALHLNPRLNIKAFVRNSFLQESWGEEERNITSFPFSPGMYFE

Exon 10 MIIYCDVREFKVAVNGVHSLEYKHRFKELSSIDTLEINGDIHLLEVRSW

FIGURE 1 (CONT'D.)

E

FAARLNTPMG PGRTVVVQGE VNANAKSFNV DLLAGKSKDI ALHLNPRLNI
KAFVRNSFLQ ESWGEEERNI TSFPFSPGMY FEMIIYCDVR EFKVAVNGVH
SLEYKHRFKE LSSIDTLEIN GDIHLLEVRS W

FIGURE 2

A

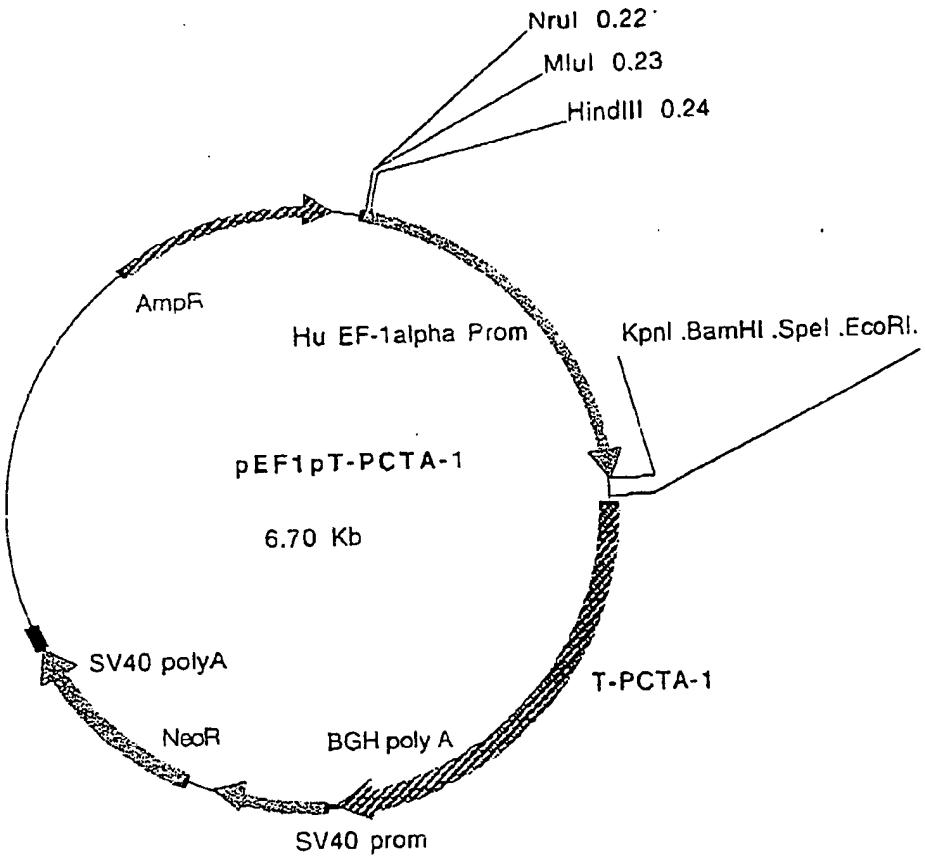

NruI 0.22
MluI 0.23
HindIII 0.24
AmpR
Hu EF-1alpha Prom
KpnI .BamHI .SpeI .EcoRI.
pEF1pT-PCTA-1
6.70 Kb
SV40 polyA
T-PCTA-1
NeoR
BGH poly A
SV40 prom

FIGURE 2 (CONT'D.)

B

MMLSLNNLQN IIYNPVIPFV GTIPDQLDPG TLIVIRGHVP SDADRFQVDL QNGSSMKPRA DVAFHFNPRF KRAGCIVCNT LINEKWGREE ITYDTPFKRE KSFEIVIMVL KDKFQVAVNG KHTLLYGHRI GPEKIDTLGI YGKVNIHSIG FSFSSDLQST QASSLELTEI SRENVPKSGT PQL

C

```
1/1                                             31/11
ATG ATG TTG TCC TTA AAC AAC CTA CAG AAT ATC ATC TAT AAC CCG GTA ATC CCG TTT GTT
Met met leu ser leu asn asn leu gln asn ile ile tyr asn pro val ile pro phe val
61/21                                           91/31
GGC ACC ATT CCT GAT CAG CTG GAT CCT GGA ACT TTG ATT GTG ATA CGT GGG CAT GTT CCT
gly thr ile pro asp gln leu asp pro gly thr leu ile val ile arg gly his val pro
121/41                                          151/51
AGT GAC GCA GAC AGA TTC CAG GTG GAT CTG CAG AAT GGC AGC AGC ATG AAA CCT CGA GCC
ser asp ala asp arg phe gln val asp leu gln asn gly ser ser met lys pro arg ala
181/61                                          211/71
GAT GTG GCC TTT CAT TTC AAT CCT CGT TTC AAA AGG GCC GGC TGC ATT GTT TGC AAT ACT
asp val ala phe his phe asn pro arg phe lys arg ala gly cys ile val cys asn thr
241/81                                          271/91
TTG ATA AAT GAA AAA TGG GGA CGG GAA GAG ATC ACC TAT GAC ACG CCT TTC AAA AGA GAA
leu ile asn glu lys trp gly arg glu glu ile thr tyr asp thr pro phe lys arg glu
301/101                                         331/111
AAG TCT TTT GAG ATC GTG ATT ATG GTG CTG AAG GAC AAA TTC CAG GTG GCT GTA AAT GGA
lys ser phe glu ile val ile met val leu lys asp lys phe gln val ala val asn gly
361/121                                         391/131
AAA CAT ACT CTG CTC TAT GGC CAC AGG ATC GGC CCA GAG AAA ATA GAC ACT CTG GGC ATT
lys his thr leu leu tyr gly his arg ile gly pro glu lys ile asp thr leu gly ile
421/141                                         451/151
TAT GGC AAA GTG AAT ATT CAC TCA ATT GGT TTT AGC TTC AGC TCG GAC TTA CAA AGT ACC
tyr gly lys val asn ile his ser ile gly phe ser phe ser ser asp leu gln ser thr
481/161                                         511/171
CAA GCA TCT AGT CTG GAA CTG ACA GAG ATA AGT AGA GAA AAT GTT CCA AAG TCT GGC ACG
gln ala ser ser leu glu leu thr glu ile ser arg glu asn val pro lys ser gly thr
541/181
CCC CAG CTT
pro gln leu
```

FIGURE 2 (CONT'D.)

D

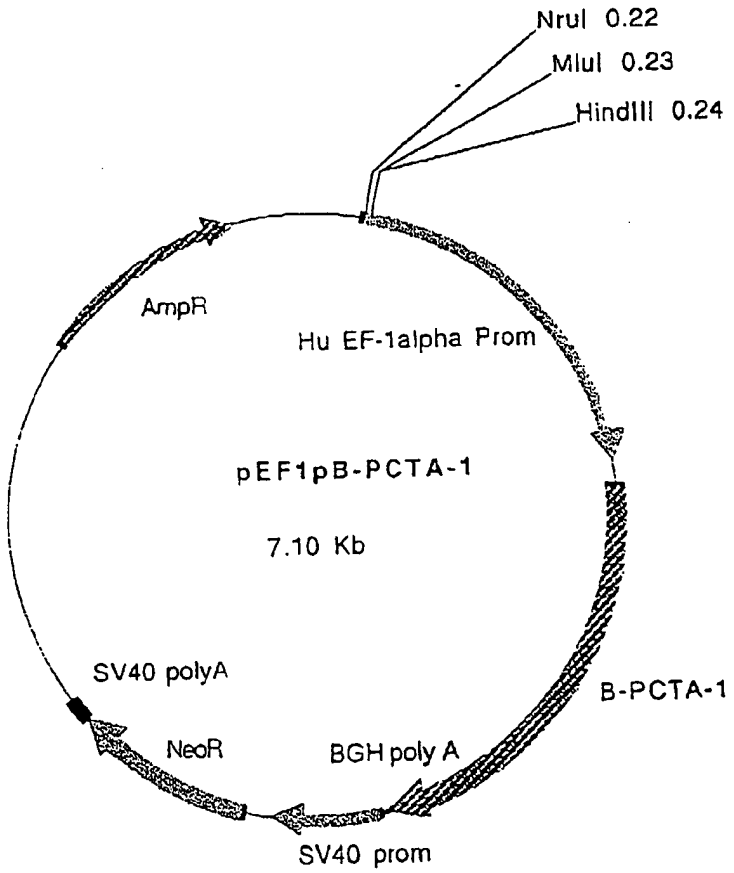


FIGURE 3

A

```
   1  AGTAAGCAGC CAGCCATTCC AAGTGGTTGA CATGACTTTG TTTAACTTTA
  51  TTTGTATTTC TGGCTGGTGT GTTTACAGCC AATAGGTCAA ACTATCAGTC
                    Putative TATA Box
 101  AGTGTAGGGC CCTGAGAAGT CGGG TATTTA AGAGCATCTA ATAGGCACAG
                          +1 Transcription initiation site
 151  AATTGTGCTC CATACTGCTT AAA CTGTTCC CTAAGTGTCC AATTTGGAGA
 201  AAACACCCAC ACGCAGGATA ACCGGCGAGT GACGCGGAGT GGCTGCGAGT
 251  CCAAGTTATC ACTAACGGAT GGGGAGCTTG GGCTGGGCAC AGTCCAGCGT
 301  ACTGAACCCT TCCCCCACCG TTTCACCTGC ATACAGAGGT GTGTACTGTC
 351  AAAAAGCAGC GCCTCCAAGT CTCTTCTGGC ACTGTCTGGA CTTGGATCCG
 401  AGGCAGACGA GGAAGCTGAG AAAACCCTGG CGTTGACCCC GTGGACCTGG
 451  GCGCCCCGGG AAGGCCAGCG CTTGGTCCAG GCAGGCGGGG CCTGTGCGGT
 501  GACCACCCTG GTCCTGAAAA GTCCCAGCCC CGAGCGCCCT CCCTCCTAGA
 551  CCTGGAGGCC TGGAACAGCC AG GTGGACGT CGGCCCACCT TTCTTTTCTT
 601  TCCTTCCCAT TTTCCTACCA CCTCCCACCC CACTCCGCCT TCCGGGCAAA
 651  GGCAGCCAGA TCCACCCAGG ACACATTCTT TGTCCTTATC CCTCTGTGCT
 701  CGTCCCACAG CAAGCCAGTC GCGGTCCAAG GCTCCAGAGG CTGTGCAGGA
 751  GGCCGAGCTG GGTGGCGATC AGCGGCGGGT CCCTGTCCAA AACCCAGCAG
 801  AGCCGCCAGG GACGCCCCAG ACACAGAAGG CGGGGCGCGG GGAGGGTGGG
 851  GAGACCACAG CAGTGAGGCG CGCGAGCCGG GAAGTGAACG AGGACTGACT
                                    ←Extension Primer
 901  CCTGTCGCTT CCGT AGCCGC CACGGACGCC AGAGCCGGGA ACCCTGACGG
 951  CACTTACTGC TGACAAACAA CCTGCTCCGT GGAGCGCCTG AAACCCAATC
1001  TTTGG GTGAG TCGCGCGAC
```

B

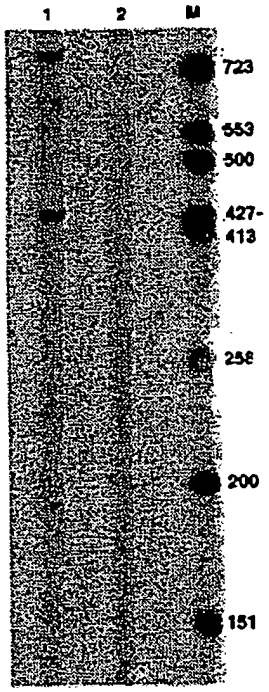


FIGURE 4

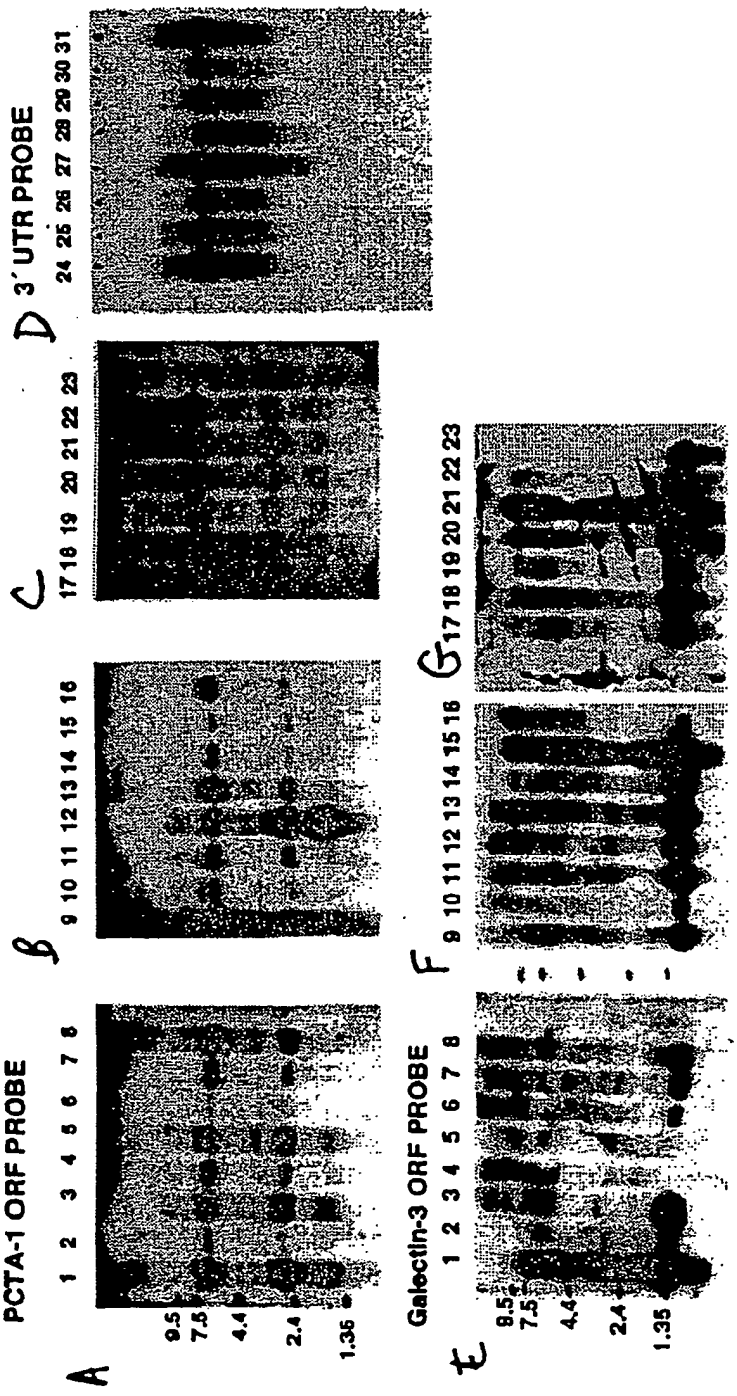

A
PCTA-1 ORF PROBE
1 2 3 4 5 6 7 8
9.5
7.5
4.4
2.4
1.35
B
9 10 11 12 13 14 15 16
C
17 18 19 20 21 22 23
D
3'UTR PROBE
24 25 26 27 28 29 30 31
E
Galectin-3 ORF PROBE
1 2 3 4 5 6 7 8
8.5
7.5
4.4
2.4
1.35
F
9 10 11 12 13 14 15 16
G
17 18 19 20 21 22 23

FIGURE 5

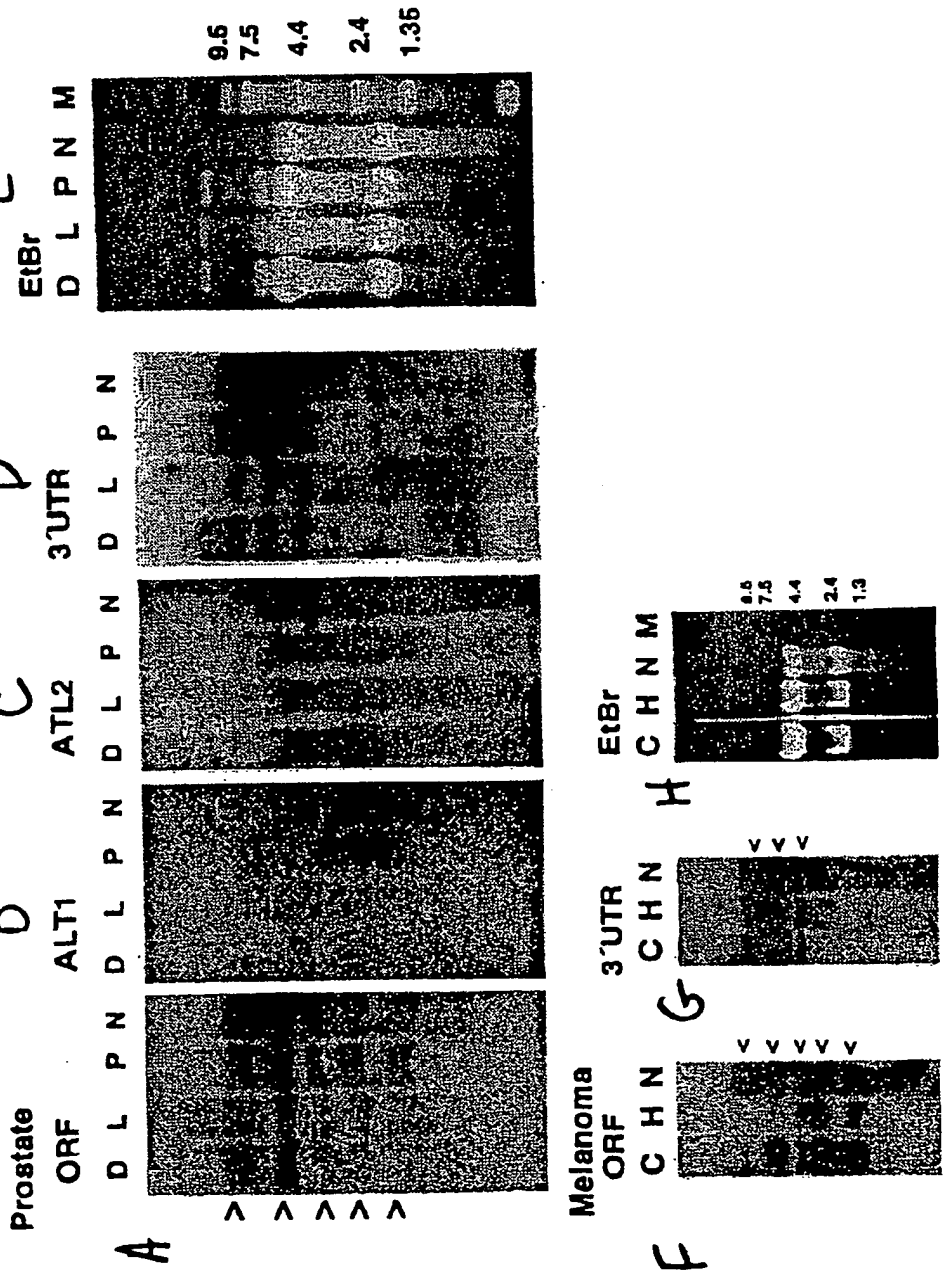

A
Prostate
ORF
D L P N
B
ALT1
D L P N
C
ATL2
D L P N
D
3'UTR
D L P N
E
EtBr
D L P N M
9.5
7.5
4.4
2.4
1.35
F
Melanoma
ORF
C H N
G
3'UTR
C H N
H
EtBr
C H N M
8.5
7.5
4.4
2.4
1.3

FIGURE 6

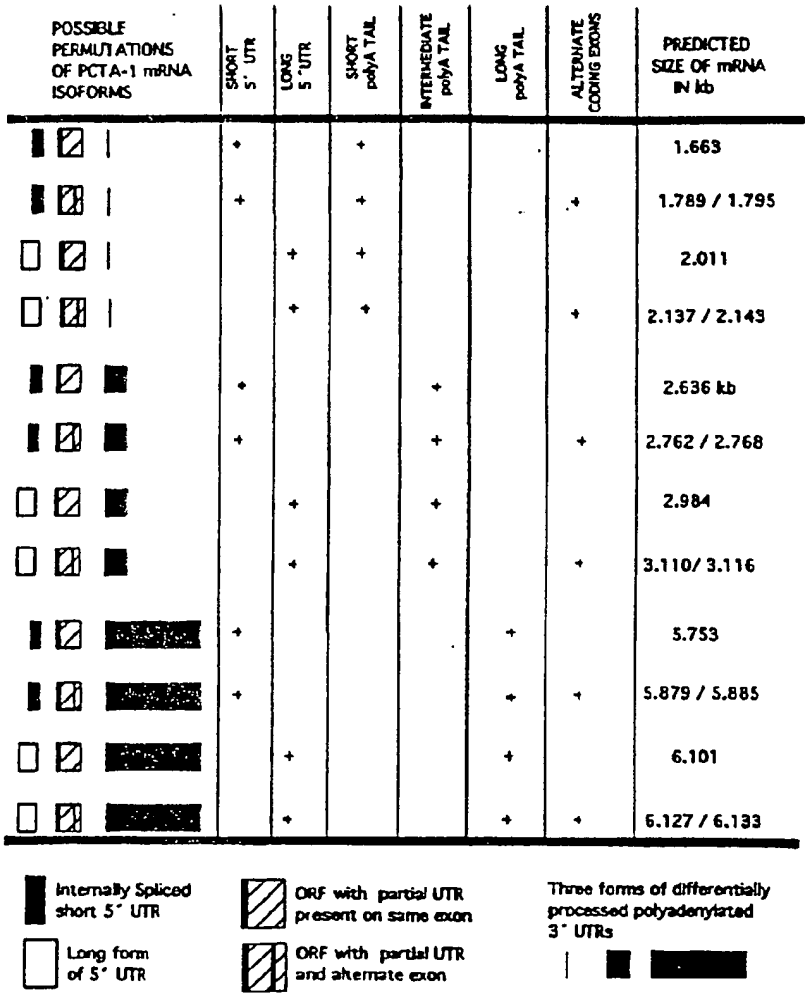

POSSIBLE PERMUTATIONS OF PCTA-1 mRNA ISOFORMS
SHORT 5' UTR
LONG 5' UTR
SHORT polyA TAIL
INTERMEDIATE polyA TAIL
LONG polyA TAIL
ALTERNATE CODING EXONS
PREDICTED SIZE OF mRNA IN kb
1.663
1.789 / 1.795
2.011
2.137 / 2.143
2.636 kb
2.762 / 2.768
2.984
3.110/ 3.116
5.753
5.879 / 5.885
6.101
6.127 / 6.133
Internally Spliced short 5' UTR
Long form of 5' UTR
ORF with partial UTR present on same exon
ORF with partial UTR and alternate exon
Three forms of differentially processed polyadenylated 3' UTRs

FIGURE 7

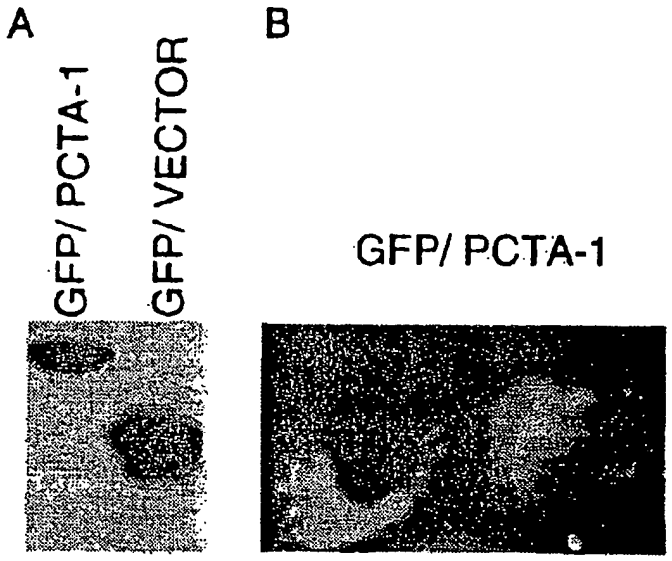


FIGURE 8

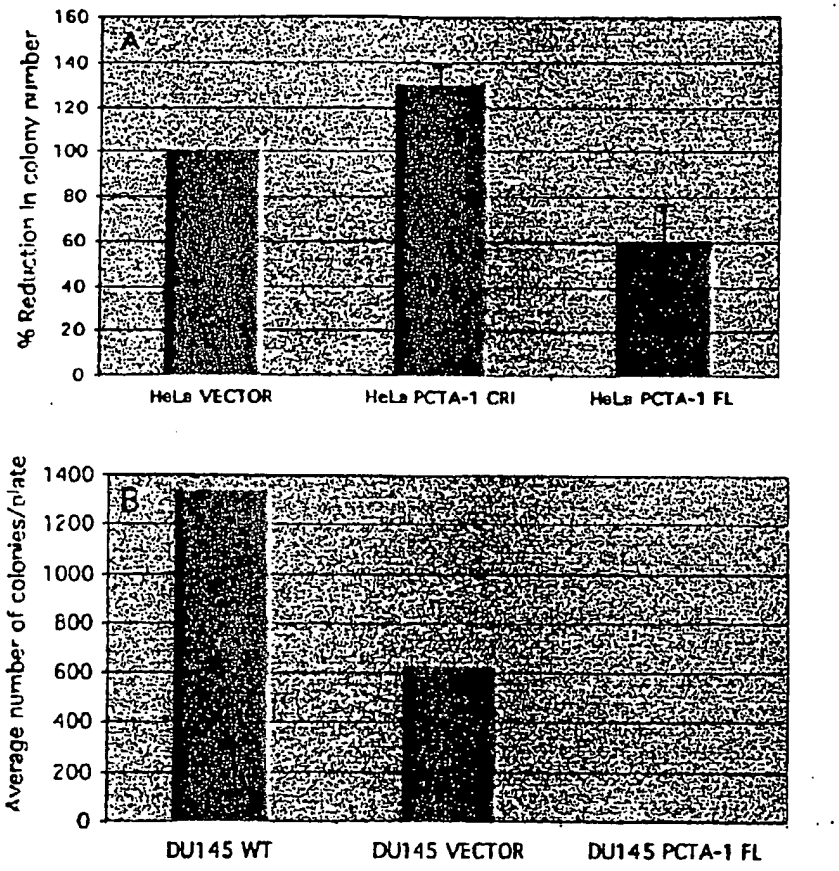

A
% Reduction in colony number
160
140
120
100
80
60
40
20
0
HeLa VECTOR
HeLa PCTA-1 CRI
HeLa PCTA-1 FL
B
Average number of colonies/plate
1400
1200
1000
800
600
400
200
0
DU145 WT
DU145 VECTOR
DU145 PCTA-1 FL

FIGURE 9

```
   1 cggcacgagc ggcacgagag aagagactcc aatcgacaag aagctggaaa agaatgatgt
  61 tgtccttaaa caacctacag aatatcatct ataacccggt aatcccgttt gttggcacca
 121 ttcctgatca gctggatcct ggaactttga ttgtgatacg tgggcatgtt cctagtgacg
 181 cagacagatt ccaggtggat ctgcagaatg gcagcagcgt gaaacctcga gccgatgtgg
 241 cctttcattt caatcctcgt ttcaaaaggg ccggctgcat tgtttgcaat actttgataa
 301 atgaaaaatg gggacgggaa gagatcacct atgacacgcc tttcaaaaga gaaaagtctt
 361 ttgagatcgt gattatggtg ctgaaggaca aattccaggt ggctgtaaat ggaaaacata
 421 cctgctcta tggccacagg atcggcccag agaaaataga cactctgggc atttatggca
 481 aagtgaatat tcactcaatt ggtttttagct tcagctcgga cttacaaagt acccaagcat
 541 ctagtctgga actgacagag atagttagag aaaatgttcc aaagtctggc acgccccagc
 601 ttagcctgcc attcgctgca aggttgaaca cccccatggg ccctggacga actgtcgtcg
 661 ttcaaggaga agtgaatgca aatgccaaaa gctttaatgt tgacctacta gcaggaaaat
 721 caaaggatat tgctctacac ttgaacccac gcctgaatat taaagcattt gtaagaaatt
 781 cttttcttca ggagtcctgg ggagaagaag agagaaatat tacctctttc ccatttagtc
 841 ctgggatgta ctttgagatg ataatttatt gtgatgttag agaattcaag gttgcagtaa
 901 atggcgtaca cagcctggag tacaaacaca gatttaaaga gctcagcagt attgacacgc
 961 tggaaattaa tggagacatc cacttactgg aagtaaggag ctggtagcct acctacacag
1021 ctgctacaaa aaccaaaata cagaatggct tctgtgatac tggccttgct gaaacgcatc
1081 tcactggtca ttctattgtt tatattgtta aaatgagctt gtgcaccatt aggtcctgct
1141 gggtgttctc agtccttgcc atgacgtatg gtggtgtcta gcactgaatg gggaaactgg
1201 gggcagcaac acttatagcc agttaaagcc actctgccct ctctcctact ttggctgact
1261 cttcaagaat gccattcaac aagtatttat ggagtaccta ctataataca gtagctaaca
1321 tgtattgagc acagattttt tttggtaaat ctgtgaggag ctaggatata tacttggtga
1381 aacaaaccag tatgttccct gttctcttga gcttcgactc ttctgtgcgc tactgctgcg
1441 cactgctttt tctacaggca ttacatcaac tcctaagggg tcctctggga ttagttatgc
1501 agatattaaa tcacccgaag acactaactt acagaagaca caactccttc cccagtgatc
1561 actgtcataa ccagtgctct gccgtatccc atcactgagg actgatgttg actgacatca
1621 ttttctttat cgtaataaac atgtggctct attagctgca agctttacca agtaattggc
1681 atgacatctg agcacagaaa ttaagccaaa aaaccaaagc aaaacaaata catggtgctg
1741 aaattaactt gatgccaagc ccaaggcagc tgatttctgt gtatttgaac ttacccgaaa
1801 tcagagtcta cacagacgcc tacagaagtt tcaggaagag ccaagatgca ttcaatttgt
1861 aagatattta tggccaacaa agtaaggtca ggattagact tcaggcattc ataaggcagg
1921 cactatcaga aagtgtacgc caactaaggg acccacaaag caggcagagg taatgcagaa
1981 atctgttttg ttcccatgaa atcaccaatc aaggcctccg ttcttctaaa gattagtcca
2041 tcatcattag caactgagat caaagcactc ttccacttta cgtgattaaa atcaaacctg
2101 tatcagcaag ttaaatggtt ccatttctgt gatttttcta ttatttgagg ggagttggca
2161 gaagttccat gtatatggga tctttacagg tcagatcttg ttacaggaaa tttcaaaggt
2221 ttgggagtgg ggagggaaaa aagctcagtc agtgaggatc attccacatt agactggggc
2281 agaactctgc caggatttag gaatattttc agaacagatt ttagatatta tttctatcca
2341 tatattgaaa aggaatacca ttgtcaatct tatttttta aaagtactca gtgtagaaat
2401 cgctagccct taattctttt ccagcttttc atattaatgt atgcagagtc tcaccaagct
2461 caaagacact ggttgggggt ggagggtgcc acagggaaag ctgtagaagg caagaagact
2521 cgaggaatccc ccagagttat ctttctccat aaagaccatc agagtgctta actgagctgt
2581 tggagactgt gaggcattta ggaaaaaaat agcccactca catcattcct tgtaagtctt
2641 aagttcattt tcattttacg tggaggaaaa aaatttaaaa agctattagt atttattaat
2701 gaattttact gagacatttc ttagaaatat gcacttctat actagcaagc tctgtctcta
2761 aaatgcaagt tggcctttg cttgccacat ttctgcatta aacttctata ttagcttcaa
2821 aggcttttaa tctcaatgcg aacattctac gggatgttct tagatgcctt taaaaagggg
2881 gcaagatcta attttatttg aaccctcact ttccaacttt caccatgacc cagtactaga
2941 gattagggca cttcaaagca ttgaaaaaaa tctactgata cttacttttct tagacaagta
3001 gttcttagtt aaccaccaat ggaactgggt tcattctgaa tcctggagga gcttcctcgt
3061 gccacccagt gtttctgggc cctctgtgtg agcagccagg tgtgagctgt tttagaagca
3121 gcgtgttgcc ttcatctctc ccgtttccca aaagaacaaa ggataaaggt gacagtcaca
3181 ctcctgggtt aaaaaaagca ttccagaacc acttctcttt atgggcacaa caacaaagaa
3241 gctaagttcg cctacccaaa tgaaagtagg ctttacagtc aagtacttct gttgattgct
3301 aaataacttc attttcttga aatagagcaa ctttgagtga aatctgcaac atggatacca
3361 tgtatgtaag atactgctgt acagaagagt taaggcttac agtgcaaatg aggcgtcagc
```

FIGURE 9 (CONT'D.)

```
3421 tttgggtgct aaaattaaca agtctaatat tattaccatc aatcaggaag agataataaa
3481 tgtttaaaca aacacagcag tctgtataaa aatacgtgta tatttactct ttctgtgcac
3541 gctctatagc ataggcagga gaggcttatg tggcagcaca agccaggtgg ggattttgta
3601 aagaagtgat aaaacatttg taagtaatcc aagtaggaga tattaaggca ccaaaagtaa
3661 catggcaccc aacacccaaa aataaaaata tgaaatatga gtgtgaactc tgagtagagt
3721 atgaaacacc acagaaagtc ttagaaatag ctctggagtg gctctcccag gacagtttcc
3781 agttggctga atagtctttt ggcactgatg ttctacttct tcacattcat ctaaaaaaaa
3841 aaaaaaaaaa
```

FIGURE 10

MMLSLNNLQNIIYNPVIPFVGTIPDQLDPGTLIVIRGHVPSDADRFQVDLQNGSSVKPRADVAFHFNPRFKR
AGCIVCNTLINEKWGREEITYDTPFKREKSFEIVIMVLKDKFQVAVNGKHTLLYGHRIGPEKIDTLGIYGK
VNIHSIGFSFSSDLQSTQASSLELTEIVRENVPKSGTPQLSLPFAARLNTPMGPGRTVVVQGEVNANAKSF
NVDLLAGKSKDIALHLNPRLNIKAFVRNSFLQESWGEEERNITSFPFSPGMYFEMIIYCDVREFKVAVNGV
HSLEYKHRFKELSSIDTLEINGDIHLLEVRSW

FIGURE 11

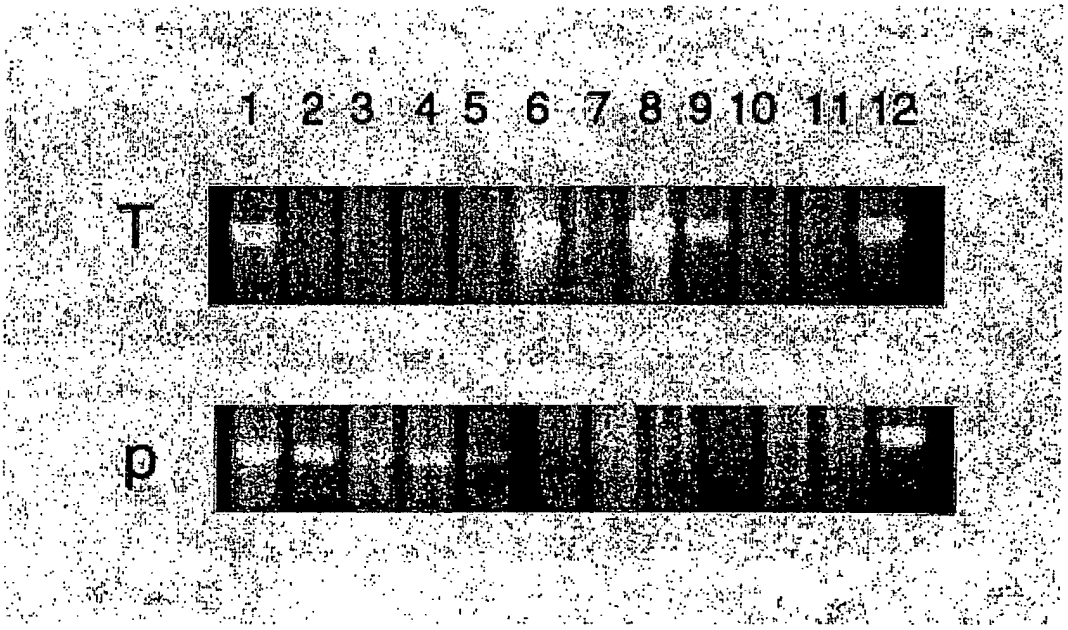
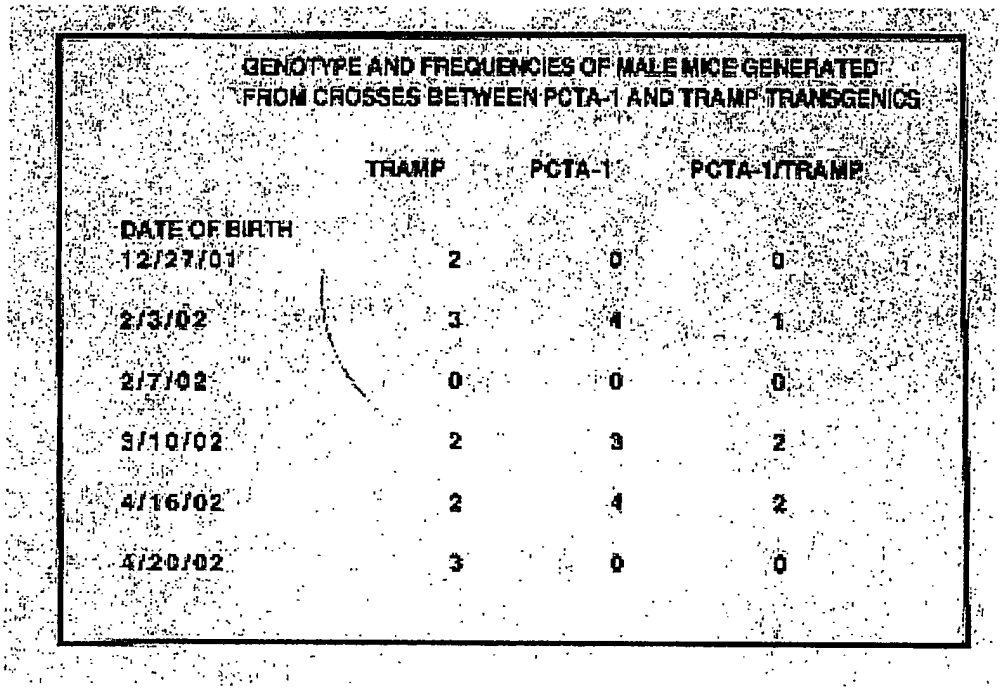


FIGURE 12



GENOTYPE AND FREQUENCIES OF MALE MICE GENERATED FROM CROSSES BETWEEN PCTA-1 AND TRAMP TRANSGENICS

DATE OF BIRTH	TRAMP	PCTA-1	PCTA-1/TRAMP
12/27/01	2	0	0
2/3/02	3	4	1
2/7/02	0	0	0
3/10/02	2	3	2
4/16/02	2	4	2
4/20/02	3	0	0

FIGURE 13